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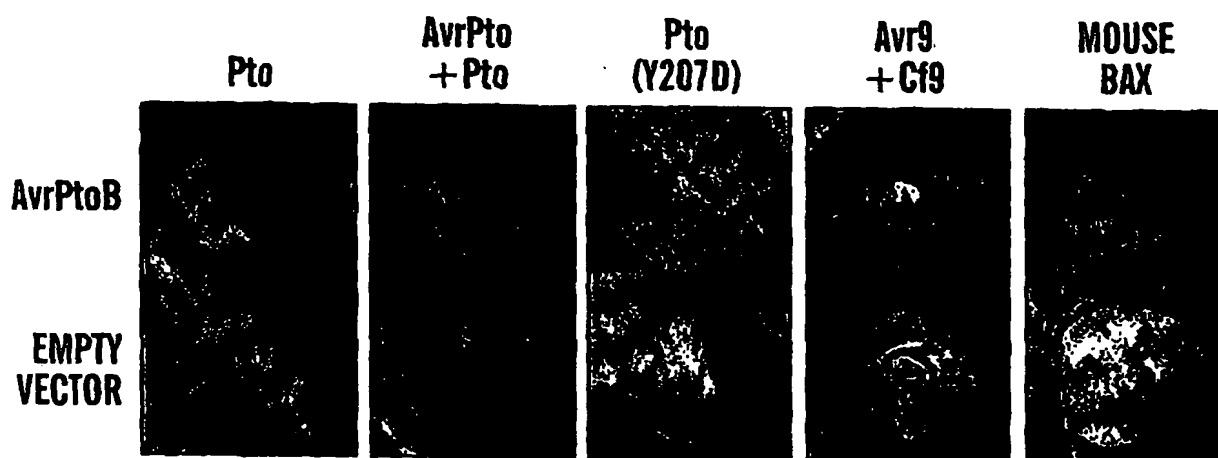


FIG. 1A



FIG. 1B

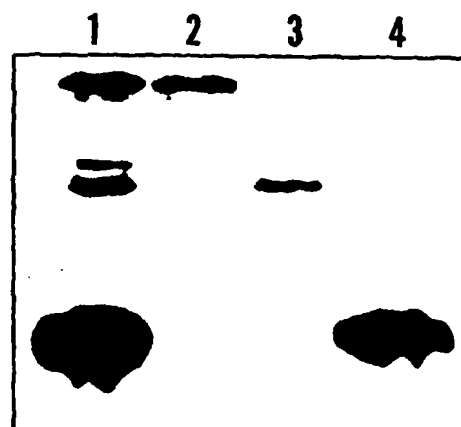


FIG. 1C

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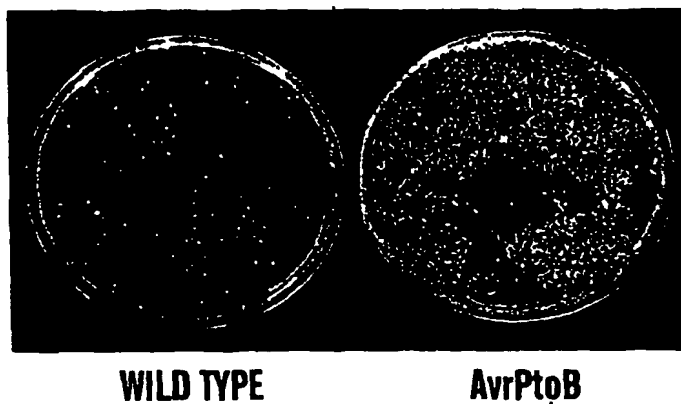


FIG. 2A

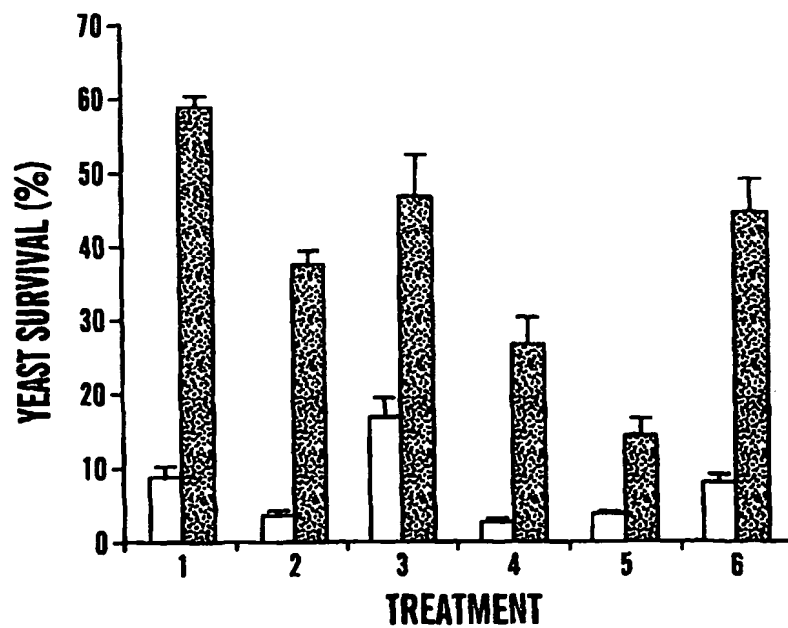
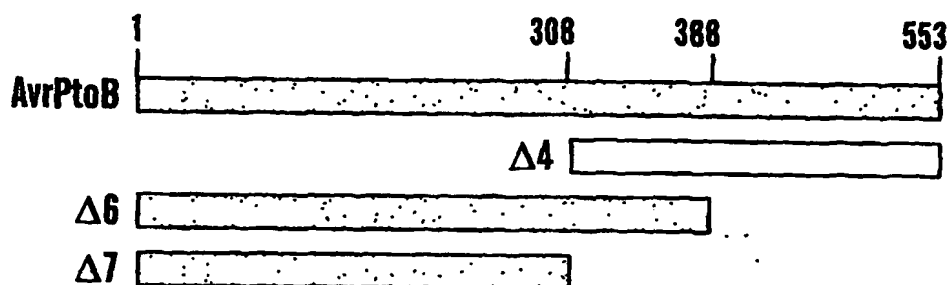


FIG. 2B

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**FIG. 3A**

	RG-PtoR (Pto/Pto, Prf/Prf)	RG-Prf3 (Pto/Pto, Prf3/Prf3)	RG-Pto11 (pto11/pto11, Prf/Prf)	RG-ptoS (pto/pto, Prf/Prf)
AvrPtoB	+	-	-	-
Δ4	-	-	-	-
Δ6	+	-	+	-*
Δ7	+	-	-	-

FIG. 3B

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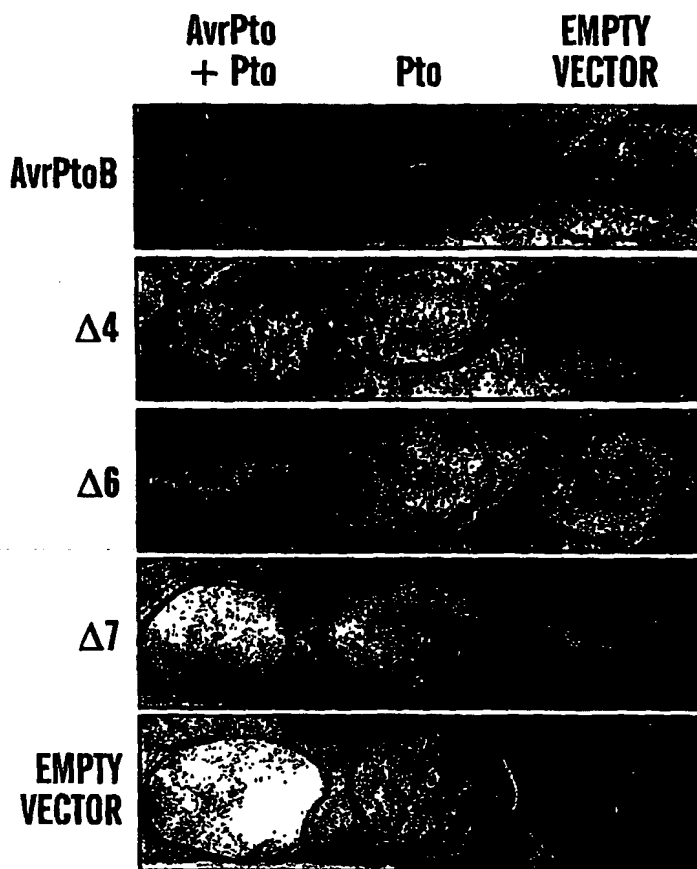


FIG. 4A

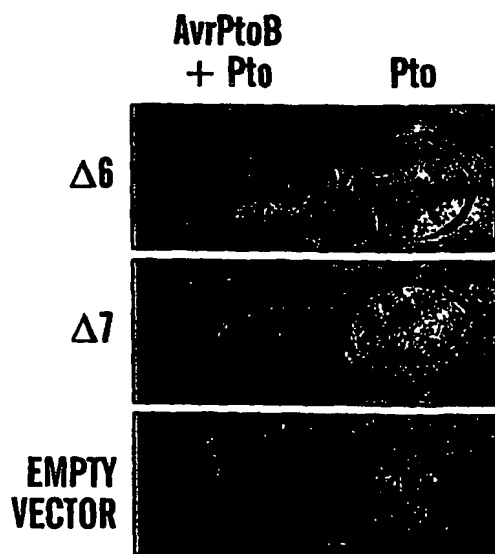


FIG. 4B

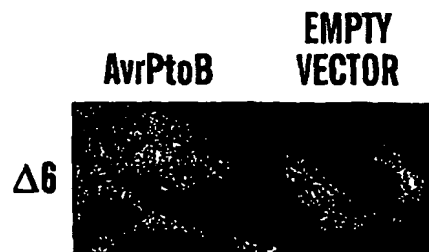
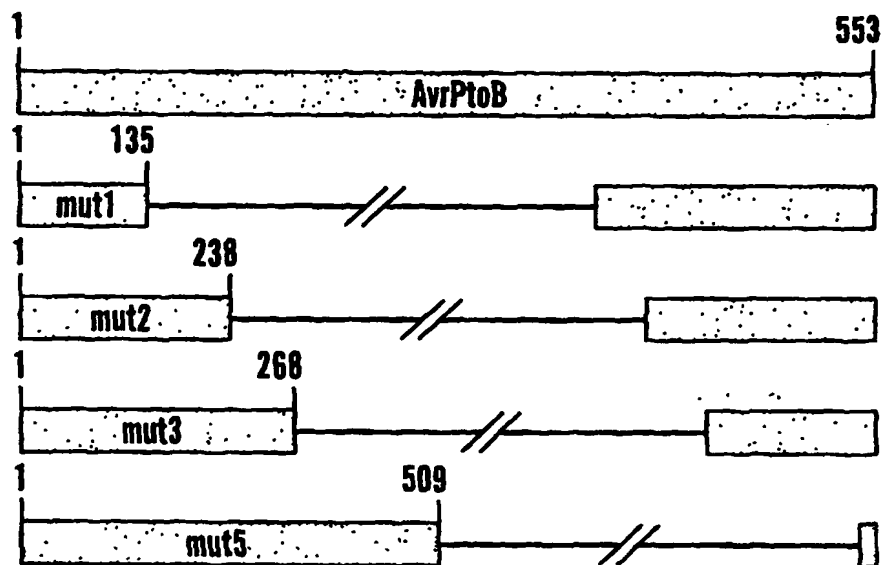


FIG. 4C

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**FIG. 5A**

	RG-PtoR (Pto/Pto, Prf/Prf)	RG-prf3 (Pto/Pto, prf3/prf3)	RG-pto11 (pto11/pto11, Prf/Prf)	RG-ptoS (pto/pto, Prf/Prf)
AvrPtoB	I	D	D	D
mut1	I	D	D	D
mut2	I	D	D	D
mut3	I	D	D	D
mut5	I	D	I	D

FIG. 5B

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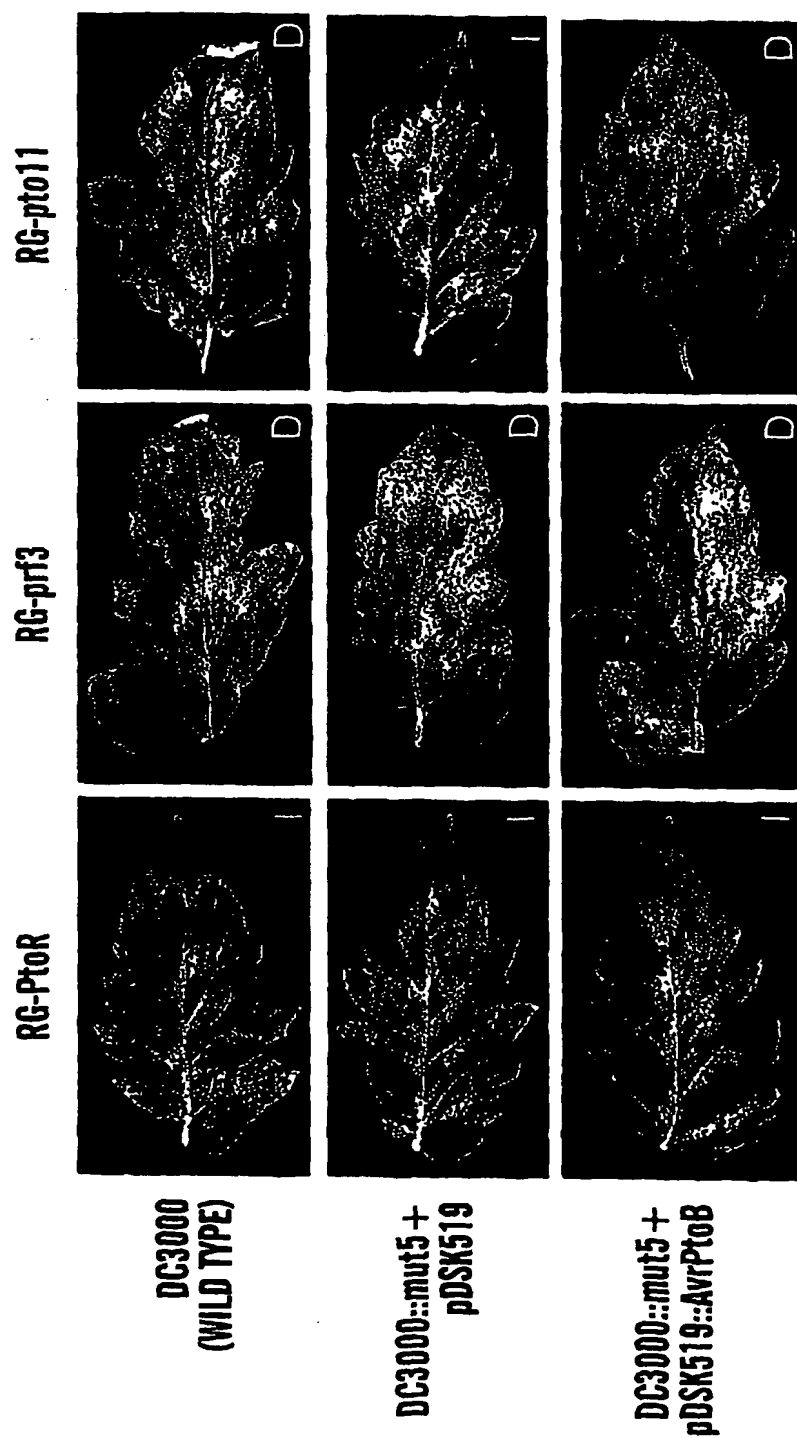


FIG. 6A

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- DC3000
- DC3000::mut5 + pDSK519
- ▼ DC3000::mut5 + pDSK519::avrPtoB

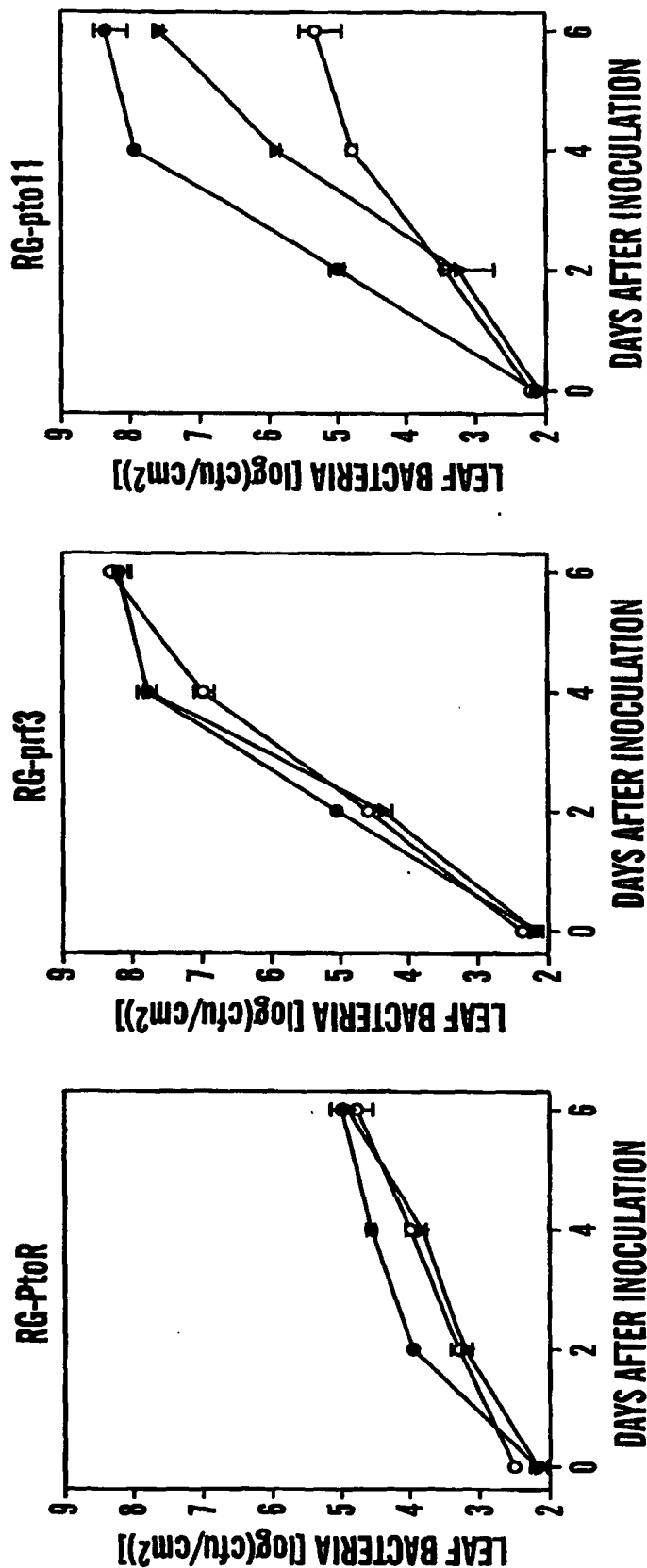


FIG. 6B

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M A G I N G A G P S G A Y F V G H T D P Majority										- R E M L L R A R P L S R Q T R E W V A Majority									
10										70									
M A G I N R A G P S G A Y F V G H T D P	DC3000									G R E L S R S T A L S R Q T R E W L E	DC3000								
M A G I N G A G P S G A Y F V G H T D P	T1									- R E M L L R A R P L S R Q T R E W V A	T1								
M A G I N G A G P S G A Y F V G H T D P	PT23									- R E M L L R A R P L S R Q T R E W V A	PT23								
M A G I N G A G P S G A Y F V G H T D P	JL1065									- R E M L L R A R P L S R Q T R E W V A	JL1065								
20										80									
E P A S G G A H G S S S G A S S S N S P Majority										Q G M P P T A E A G V P I R P Q E S A E Majority									
30										90									
E P V S G Q A H G S S G A S S S N S P	DC3000									Q G M P T A E D A S V R R R R P P Q V T A D	DC3000								
E P A S G G A H G S S S G A R S S N S P	T1									Q G M P P T A E A G V P I R P P Q E S A E	T1								
E P A S G G A H G S S S G A S S S N S P	PT23									Q G M P P T A E A G V P I R P P Q E S A E	PT23								
E P A S G G A H G S S S G A S S S N S P	JL1065									Q G M P P T A E A G V P I R P P Q L S A E	JL1065								
40										100									
R L - P A P P D A P A S Q A R D R - - - Majority										A A P Q A R A E E R H T P E A D A A A Majority									
50										110									
Q V Q P R P S N T P P S N A P A P P T	DC3000									A A T P - - R A E A R R T P E A T A D A	DC3000								
R L - P A P P D A P A S Q A R D R - - -	T1									A A A P Q A R A L E R H I P E A D A A A	T1								
R L - P A P P D A P A S Q A R D R - - -	PT23									A A A P Q A R A L E R H T P E A D A A A	PT23								
R L - P A P P D A P A S Q A R D R - - -	JL1065									A A A P Q A R A L E R H T P E A D A A A	JL1065								
60										120									

FIG. 7A

PCT/US2003/025247

FIG. 7B

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RSTVPPPTSTESSSSGNQRTL Majority		-GANRVVMRRNHGNN EADA - Majority	
215	---PASPAA	250	260
236	RSTVPPPTSTLSSSSGNQRTL	268	-RVDRAAMRRNRGNDEADA - DC3000
236	RSTVPPPTSTLSSSSGNQRTL	296	-GANRVVMRRNHGNN EADA - T1
236	RSTVPPPTSTLSSSSGNQRTL	296	-GANRVVMRRNHGNN EADA - PT23
236	RSTVPPPTSTLSSSSGNQRTL	296	-GANRVVMRRNHGNN EADA - JL1065
LGRFAGLMTPNQRRPSSASN Majority		ALQGLAQQGVDMEDLRAALE Majority	
231	FCRFA RLWAPNQGRS - - - N	330	340
256	LGRFAGLWIPNQRRPSSASN	285	ALRGLVQQGVNL EHLRTALE DC3000
256	LGRFAGLWIPNQRRPSSASN	313	ALQGLAQQGVDMEDLRAALE T1
256	LGRFAGLWIPNQRRPSSASN	313	ALQGLAQQGVDMEDLRAALE PT23
256	LGRFAGLWIPNQRRPSSASN	313	ALQGLAQQGVDMEDLRAALE JL1065
ASASQRPVDRSPPRVNQVPTI Majority		RHILHRRRPIPM D IAYALQGV Majority	
248	TASQT PVDRSPPRVNQVPTI	350	360
276	ASASQRPVDRSPPRVNQVPTI	305	RHVMQRLPPLPLDI GSA LQNV DC3000
276	ASASQRPVDRSPPRVNQVPTI	333	RHILHRRRPIPM D IAYALQGV T1
276	ASASQRPVDRSPPRVNQVPTI	333	RHILHRRRPIPM D IAYALQGV PT23
276	ASASQRPVDRSPPRVNQVPTI	333	RHILHRRRPIPM D IAYALQGV JL1065

FIG. 7C

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G I A P S I D T G E S L M E N P L M N L Majority		L Q V I P A R E D Y E N N V A Y G V R L Majority	
370		430	
325	G I N P S I D L G E S L V Q H P L L N L	440	L R V M E R E D Y E N N V A Y G V R L
353	G I A P S I D T G E S L M E N P L M N L		DC3000 T1
353	G I A P S I D T G E S L M E N P L M N L		PT23
353	G I A P S I D T G E S L M E N P L M N L		JL1065
S V A L H R A L G P R P A R A Q A P R P Majority		L S L N P G A G V R E T V A A F V N N R Majority	
390		450	
345	N V A L N R M L G L R P P S A E R A P R P	460	L N L N P G V G V R Q A V A A F V T D R
373	S V A L H R A L G P R P A R A Q A P R P		DC3000 T1
373	S V A L H R A L G P R P A R A Q A P R P		PT23
373	S V A L H R A L G P R P A R A Q A P R P		JL1065
A V P V A P A T V S R R P D S A R A T R Majority		Y E R Q A V V A D I R A A L N - L S K Q Majority	
410		470	
365	A V P V A P A T A S R R R P D G T R A T R	480	A E R P A V V A N I R A A L D P I A S Q
393	A V P V A P A T V S R R R P D S A R A T R		DC3000 T1
393	A V P V A P A T V S R R R P D S A R A T R		PT23
393	A V P V A P A T V S R R R P D S A R A T R		JL1065

FIG. 7D

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F N K L R T V S K A D A A S N K P G F K Majority		S Y S R E A N K D L V F M D M K K L A Q Majority	
445	F S Q L R T I S K A D A A E S E E L G F K	505	P Y S Q L G N K D L A F M D M K K L A Q
472	F N K L R T V S K A D A A S N K P G F K	531	S Y S R E A N K D L V F M D M K K L A Q
472	F N K L R T V S K A D A A S N K P G F K	531	S Y S R E A N K D L V F M D M K K L A Q
472	F N K L R T V S K A D A A S N K P G F K	531	S Y S R E A N K D L V F M D M K K L A Q
D A A D H P - D D A T Q C L F G E E L S Majority		F L A G K P E H P M T R E T L N A E N I Majority	
465	D A A D H T U D V T H C L F G G E L S	525	F L A G K P E H P M T R E T L N A E N I
492	D A A D H P - D D A T Q C L F G E E L S	551	F L A G K P E H P M T R E T L N A E N I
492	D L A D H P - D D A T Q C L F G E E L S	551	F L A G K P E H P M T R E T L N A E N I
492	D L A D H P - D D A T Q C L F G E E L S	551	F L A G K P E H P M T R E T L N A E N I
L T S S V Q Q V I G L A G K A T D M S E Majority		A K Y A F R I V P - Majority	
485	L S N P D Q Q V I G L A G N P T D T S Q	545	A K Y A F R I V P .
511	L T S S D Q Q V I G L A G K A T D M S E	571	A K Y A F R I V P .
511	L T S S V Q Q V I G L A G K A T D M S E	571	A K Y A F R I V P .
511	L T S S V Q Q V I G L A G K A T D M S E	571	A K Y A F R I V P .

FIG. 7E

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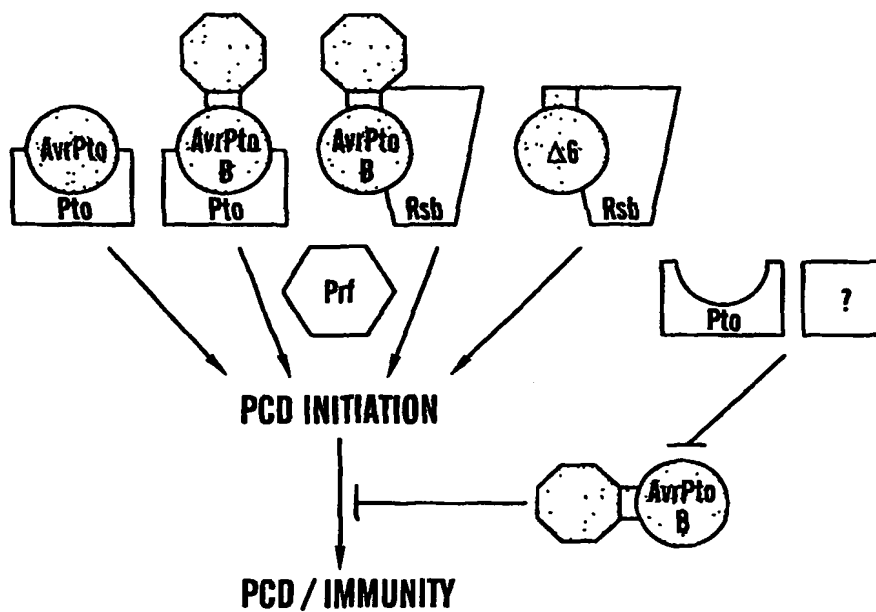


FIG. 8

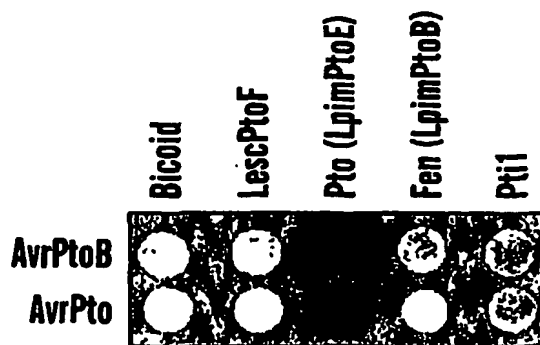


FIG. 9A

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Putative Hrp-box

```

1  ACAGTTCCCCAGGGTGAATAGGGAAAGGTGTGATGgaagccttttctgtgctcttttgcgcag
61 ACAGCGCTGATCTTGCGGGTGATTCCGGTCCGCAGGCAGAAGATCGGAGAGGATCAGCAT
121 ATGGCGGGTATCAATAGAGCGGGACCATCGGGCGCTTATTTTGTGTCACACAGACCCC
1  M A G I N R A G P S G A Y F V G H T D P
181 GAGCCAGTATCGGGGCAAGCACACGGATCCGGCAGCGGCCAGCTCCTCGAACAGTCCG
21  E P V S G Q A H G S G S G A S S S N S P
241 CAGGTTACGCCGACCCCTCGAATACTCCCCCGTCGAACGCGCCCCACCGCGCCAAAC
41  Q V Q P R P S N T P P S N A P A P P P T
301 GGACGTGAGAGGCTTTCACGATCCACGGCGCTGTGCGGCCAAACCAGGGAGTGGCTGGAG
61  G R E R L S R S T A L S R Q T R E W L E
361 CAGGGTATGCCTACAGCGGAGGATGCCAGCGTCGTCGTAGGCCACAGGTGACTGCCGAT
81  Q G M P T A E D A S V R R R P Q V T A D
421 GCCGCAACGCCGCGTGCAGAGGCAAGACGCACGCCGGAGGCAACTGCCGATGCCAGCGCA
101 A A T P R A E A R R T P E A T A D A S A
481 CCGCGTAGAGGGGCGGTTGCACACGCCAAGATCGTTTCAGCAATTGGTCAGTGAGGGC
121 P R R G A V A H A N S I V Q Q L V S E G
541 GCTGATATTTGCGATACTCGTAACATGCTCCGCAATGCAATGAATGCGCAGCGAGTCGCT
141 A D I S H T R N M L R N A M N G D A V A
601 TTTTCTCGAGTAGAACAGAACATATTTTCGCCAGCATTTCCCGAACATGCCCATGCATGGA
161 F S R V E Q N I F R Q H F P N M P M H G
661 ATCAGCCGAGATTCCGAACCTCGTATCGAGCTCCGTGGGGCGCTTCGTCGAGCGGTTTAC
181 I S R D S E L A I E L C R G A L R A V H
721 CAACAGGCGGGCGTCAGCGCCAGTGAGGTGCCCCACGCCAACACCGGCCAGCCCTGCGGCA
201 Q Q A A S A P V R S P T P T P A S P A A
781 TCATCATCGGGCAGTCAGCGCTTATTGACGGTTTGGCCGTTTGTATGGCGCCA
221 S S S G S S Q R S L F G R F A R L M A P
841 AACCAGGACGGTCTGCAACACTGCCGCCTCTCAGACGCCGGTTCGACAGGAGCCCGCCA
241 N O G R S S N T A A S S Q T P V D R S P P
901 CGCGTCAACCAAAGACCCATACGCTCGACAGGGCTGCGATGCGTAATCGTGGCAATGAC
261 R V N O R P I R V D R A A M R N R G N D
961 GAGGCGGACCGCGGGCTGCGGGGTTAGTACAACAGGGGGTCAATTTAGAGCCCTGCGC
281 E A D A L R G L V Q Q G V N L E H L R
1021 ACGGCCCTTGAAAGACATGTAATGCAGCGCCTCCCTATCCCCCTCGATATAGGCAGCGG
301 T A L E R H V M Q R L P I P L D I G S A
1081 TTGAGAATGTGGGAATTAACCAAGTATCGACTTGGGGGAAAGCCTTGTGCAACATCCC
321 L Q N V G I N P S I D L G E S L V Q H P
1141 CTGCTGAATTTGAATGTAGCGTTGAATCGCATGCTGGGGCTGCGTCCCAGCGCTGAAAGA
341 L L N V A L N R M L G L R P S A E R
1201 GCGCCTCGTCCAGCGCTCCCGTCCCGGACCGCCTCCAGGCGACCGGATGGTACG
361 A P R P A V P V A P A T A S R R P D G T
1261 CGTGCAACACGATTGCGGGTGATGCCGGAGCGGGAGGATTACGAAAATAATGTGGCTTAT
381 R A T R L R V M P E R E D Y E N N V A Y
1321 GGAGTGGCTTGCTTAACCTGAACCCGGGGGTGGGGGTAAGGCAGGCTGTTGCGGCCTTT
401 G V R L L N L N P G V G V R Q A V A A F
1381 GTAACCGACCGGGCTGAGCGGCCAGCAGTGGTGGCTAATATCCGGGCAGCCCTGGACCTT
421 V T D R A E R P A V V A N I R A A L D P
1441 ATCGCGTCACAATTCAGTCAGCTGCCACAATTTCAAGGCCGATGCTGAATCTGAAGAG
441 I A S Q F S Q L R T I S K A D A E S E E
1501 CTGGGTTTAAAGGATGCGGCAGATCATCACCGATGACGTGACGCACTGCTCTTTTGGC
461 L G F K D A A D H H T D D V T H C L F G
1561 GGAGAATTGTGCTGAGTAATCCGGATCAGCAGGTGATCGGTTTGGCGGGTAATCCGACG
481 G E L S L S N P D Q Q V I G L A G N P T
1621 GACACGTCGCAGCCTTACAGCCAAGAGGGAATAAGGACCTGGCGTTTCATGGATATGAA
501 D T S Q P Y S Q E G N K D L A F M D M K
1681 AAACCTTGCCCAATTCCTCGCAGGCAAGCCTGAGCATCCGATGACCAGAGAAACGCTTAAC
521 K L A Q F L A G K P E H P M T R E T L N
1741 GCCGAAAATATCGCCAAGTATGCTTTTAGAATAGTCCCCTgaCCGCGCTGACAGCTAAAA
541 A E N I A K Y A F R I V P
1801 GCCCATCAAGCTAGCGCCGACAGCGCTCACTGCCACTTCGAAGGTGGCGGTGGAAAGCTC
1861 CCGAGTCACGGAATTCGCACCTGCGTCAGGGCTCAGTCCATGCGCTCGGGGTAGGTCATC

```

FIG. 9B

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- 52% identity of amino acid between AvrPtoB and VirPphA
- Black boxed letters: Putative hrp-box

- Red boxed letters: Computer suggested N-myristoylation site

1.	3- 8	GINRAG
2.	25- 30	GQAHGS
3.	29- 34	GSGSGA
4.	31- 36	GSGASS
5.	33- 38	GASSSN
6.	82- 87	GMPTAE
7.	140-145	GADISH
8.	278-283	GNDEAD
9.	288-293	GVSTTG
10.	294-299	GQFRAL
11.	325-330	GINPSI
12.	353-358	GLRPSA
13.	379-384	GTRATR
14.	412-417	GVRQAV
15.	480-485	GGELSL

- Black bold letters: Amino acid identical with amino acid of VirPphA

- Blue arrow: Fusion point of truncated AvrPtoB with LexA of prey vector

1.	70 AA; <i>HinP1I</i>
2.	112 AA; <i>MspI</i>
3.	121 AA; <i>AclI</i>

FIG. 9B (CONT.)

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ALIGNMENT OF THE AMINO ACID SEQUENCES OF AvrPtoB AND VirPpha

BlastX results

Sequences producing significant alignments:					Score	E
					(bits)	Value
gi	5702216	gb	AAD47203.1	AF141883_1 (AF141883) VirPpha [Pse...	500	e-140
gi	5702219	gb	AAD47206.1	AF141883_4 (AF141883) unknown [Pse...	70	6e-11
gi	7512219	pir	T18535	high molecular mass nuclear antigen ...	50	6e-05
gi	15236788	ref	NP_194968.1	(NC_003075) putative protein [...	45	0.002
gi	5420387	emb	CAB46679.1	(AJ243459) proteophosphoglycan [...	45	0.003
gi	6322209	ref	NP_012284.1	(NC_001141) Required for invasi...	44	0.005
gi	14251109	ref	NP_116471.1	(NC_002794) t120 [Tupaia herpe...	43	0.008
gi	4507349	ref	NP_003176.1	(NM_003185) TATA box binding pr...	42	0.013
gi	17546705	ref	NP_520107.1	(NC_003295) PROBABLE TRANSMENB...	42	0.013
gi	15805485	ref	NP_294181.1	(NC_001263) hypothetical prote...	42	0.013
gi	17487943	ref	XP_036528.2	(XM_036528) serine/arginine re...	42	0.018

>gi|5702216|gb|AAD47203.1|AF141883_1 (AF141883) VirPpha [Pseudomonas syringae pv. phaseolicola] Length = 539

Score = 500 bits (1287), Expect = e-140
 Identities = 303/581 (52%), Positives = 368/581 (63%), Gaps = 28/581 (4%)
 Frame = +1

Query: 1 MAGINRAGPSGAYFVGHTDPEFVSGQAHSGSGASSNSPQVQPRPSNTPPSNAPAPPT 180
 MGINAGPS ++ TD EPV+ + H S ASS+NSP++ P S P +
 Sbjct: 1 MPGINGAGPSNFFWQWRTDGEFVTEREHDSSRSASSANSPELPPAS-----PAES 51

Query: 183 GRERLSRSTALSRQTREMLEQGMPTAEDASVRRRPQVTADAATPRAEARRTPEATADASA 360
 GR+RL RS+ALSRQTREMLE A A V+ ATP AEAR++PEA
 Sbjct: 52 GRQRLLRSEALSRQTREMLE-----ATPARVQ-----GATPPAEARQSPEAQ----- 93

Query: 361 PRGAVAHANSIVQQLVSEGADISHTRMLRNAMNGDAVAFSRVEQNIFRQHFPMPMHG 540
 A IVQ+LV GAD+++ R MLRN M+ +AVAFSRVE++I QHFPMPMHG
 Sbjct: 94 -----QAERIVQELVRGGADLNNVRLMLRNVMMDNAVAFSRVERDILLQHFPMPMTG 146

Query: 541 ISRDSELAIELRGALRRRAVHQQAASAPVRSPTFTPASPAASSSGSSQSLFGRFARIMAP 720
 IS DS LA ELR LR+ V QQ R + TPA A SSSGSSQSL GR LM P
 Sbjct: 147 ISSDSVLANELRQRLRQTVRQQ-----RIQSSTPARLADSSSGSSQSLIGRSTMLMTP 200

Query: 721 NQGRSSNTAASQTPVDRSPFRVNQRPIRVDRAMRNNGNDEADAALRGLVQQGVNLEHLR 900
 + SS+ AAS+T VDR P ++ R+ AA N ++ + ALR L Q+GV++E LR
 Sbjct: 201 GRSSSSSAAASRTSVDHRHPQGLDLESARLASAARHNSANQTNEALRRLTQEGVDMERLR 260

Query: 901 TALERHVMQRLPIPLDIGSALQNVGINPSIDLGESLVQHPLNLNVALNRMGLRPSAER 1080
 T+L R++M P+P D+ AL++VGINP I SLV HP+LN + ALNRML R +
 Sbjct: 261 TELGRYIMSLEPLPPDLRRALRESVGINPFIPEELSLVDHPVLNFSALNRMGLASRQTTN 320

Query: 1081 APRPAVPVAPATASRR-----PDGT---RATRLRVMPERE 1176
 +P + A + RR P + RA RL VMP +
 Sbjct: 321 SPELPPLASSAESGRRRLRLSPPLLSGQREWIEQSMRQAEFQSSRLNRAVRLAVMPPQN 380

Query: 1177 DYENNVAYGVRLNLNPGVGVQAVAFVTDRAERPAVVANIRAALDPIASQFSQSLRTIS 1356
 + E+NVAY +RL LNPG V + VA+P+TD A R VV +IRAALD IA QFSQSLRTIS
 Sbjct: 381 ENEDNVAYAIRLRLNPGADVSRVVASFITDPAARQVVDIRAALD-IAPQFSQSLRTIS 439

Query: 1357 KADAESEELGPKDAADHHTDDVTHCLFGGELSLSNPDQVIGLAGNPTDTSQPYSEQBNK 1536
 KADAESEELGP+DAAD H D+ T CLFG ELSSNPDQVIGLA NPTD QPYSEQ NK
 Sbjct: 440 KADAESEELGPRDAAD-HPDNATSCLFGEELSLSNPDQVIGLAVNPTDKPQPYSEQEVNK 498

Query: 1537 DLAFMDMKKLAQFLAGKPEHPMTRETNAENIAYAFRIVP 1659
 L FMDMKKLAQ+LA KPEHP+ R+ L+A+NIAYAF+IVP
 Sbjct: 499 ALTFMDMKKLAQVLADKPEHPMLNRQRLDAKNIAKYAFKIVP 539

FIG. 9C

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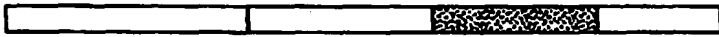


CHIMERIC		INTERACTION WITH:	
		AvrPto	AvrPtoB
A		YES	YES
B		NO	NO
D		NO	NO
E		NO	NO
F		NO	NO
G		YES	YES
H		NO	NO

FIG. 10A


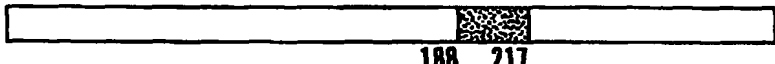
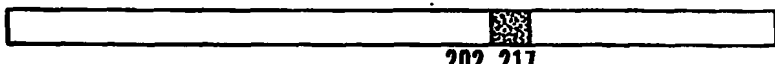
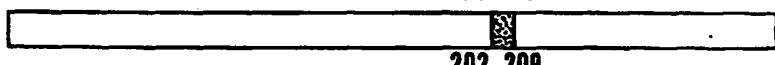
		INTERACTION WITH:	
		AvrPto	AvrPtoB
FPB		YES	YES
FPB2		YES	YES
FPB3		YES	YES
FPB4		YES	YES

FIG. 10B














		INTERACTION WITH:	
		AvrPto	AvrPtoB
Pto		YES	YES
Fen		NO	NO
FPB3		YES	YES
FPB4		YES	YES
FPB3(K202R)		YES	YES
FPB3(T204N)		NO	NO
FPB3(L205I)		YES	YES
FPB3(D209A)		YES	YES
P(T204N)		NO	NO
P(L205I)		YES	YES
F(N204T,1205L)		YES	YES
F(N204T)		YES	YES
F(1205L)		NO	NO

FIG. 10C

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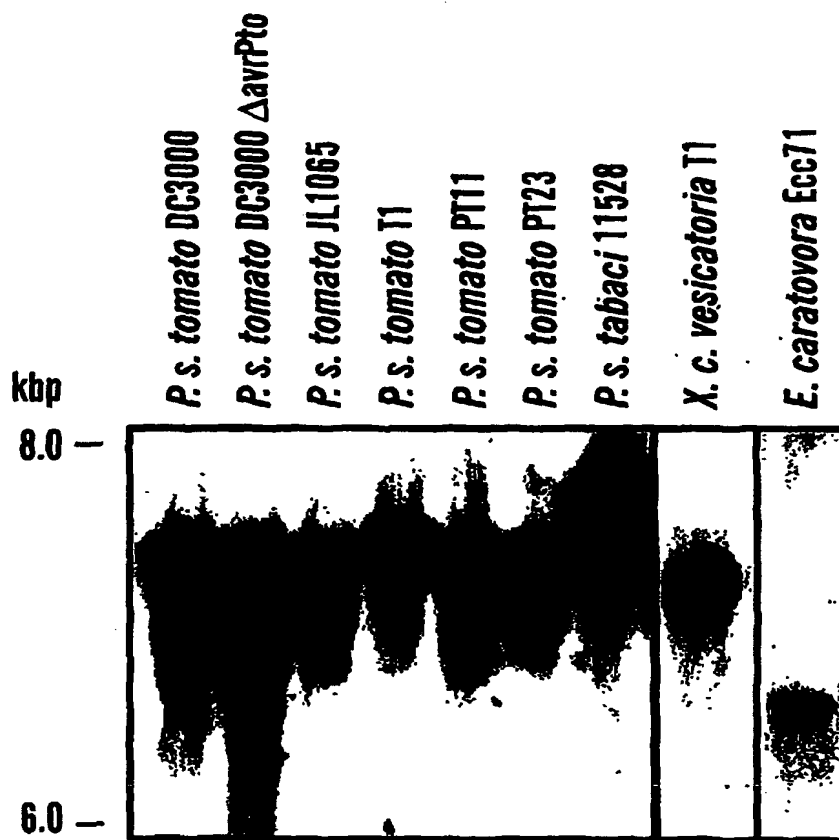


FIG. 11

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P. fluorescens (Hrp+, avrPtoB)

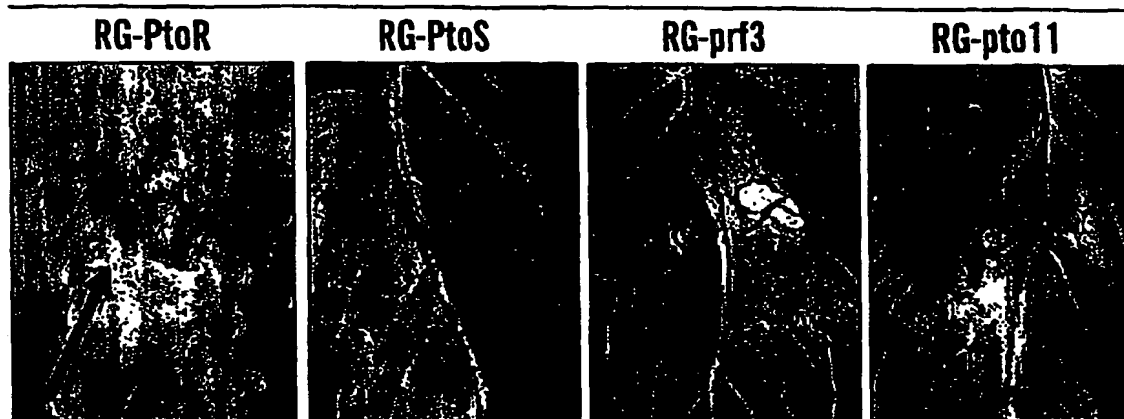


FIG. 12A

Agrobacterium (35S::avrPtoB)

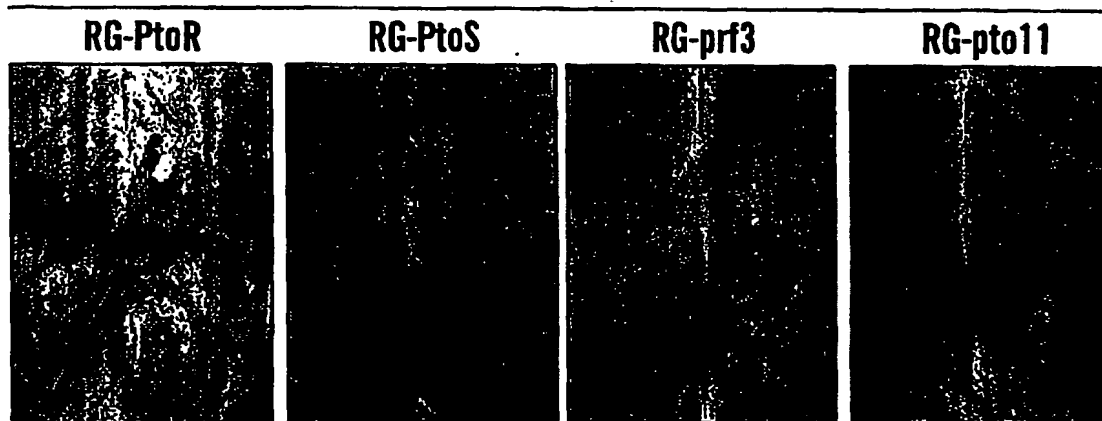
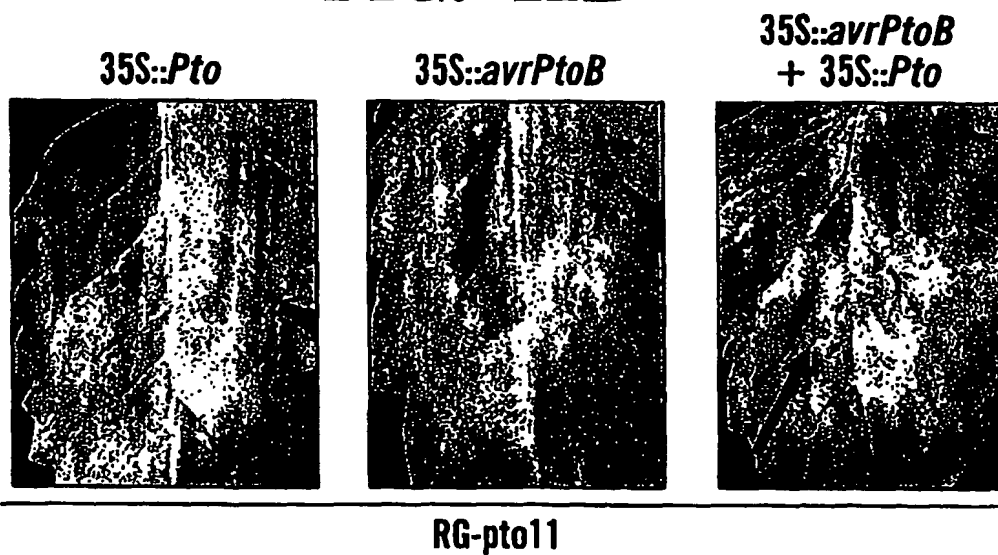


FIG. 12B



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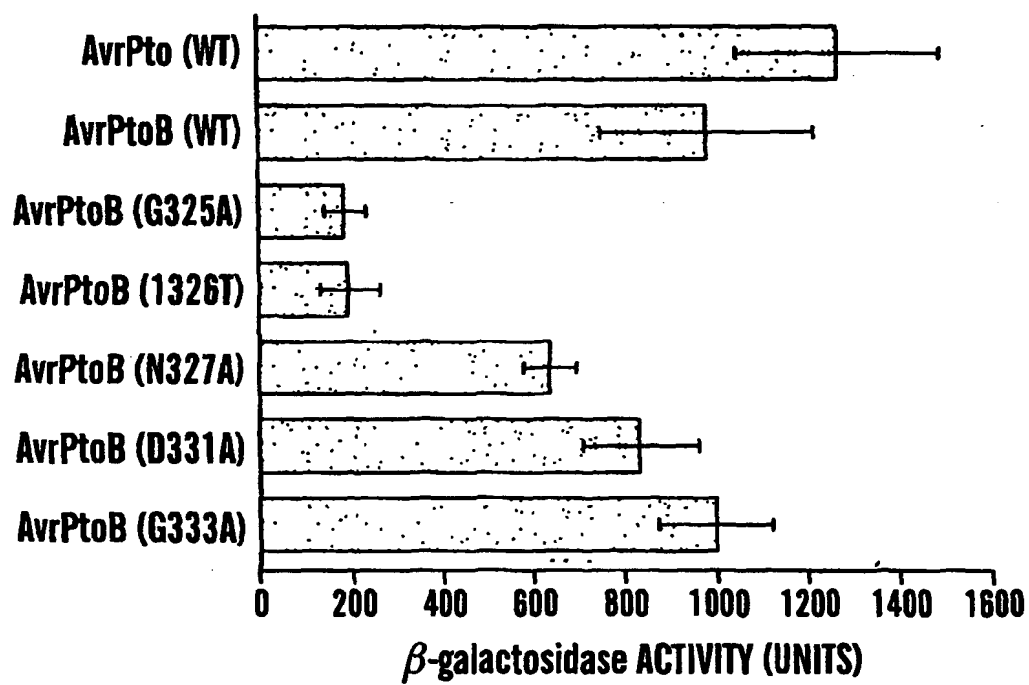
		Subregion
MAGINRAGPSGAYFVGHTDPEFVSGQAHGSGSGASSNSPQVQPRPSNTP MGNICVGG-----SRMAHQVNSPDRVSNNSGDE		I, II
PSNAPAPPPTGRERLSRSTALSRQTREWLEQGMPAEDASVRRRPQVTAD DNVTSSQLLSVRHQLAESAGLPRDQHEFVSSQAP----QSLRNR----- NA121↓ AATPRAEARRTPEATADASAPRRGAVAHANSIVQQLVSEGADISHTRNML -----YNNL-----		III
RNAMNGDAVAFSRVEQNIIFRQHFPNMPMHGISRDSELAIELRGALRRVH -----YSHQTORTLDMADMQHRYMTGAS----- ●		IV
QQAASAFVRSPTPTPASPAASSSGSSQRSIFGRFARLMAPNQGRSSNTAA -----		
SQTPVDRSPFRVNQRPIRVDRAMRNRGNDADAALRGLVQQGVNLEHLR -----		
TALERHVMQRLPIPLDIGSALQNVGINPSIDLGESLVQHPLLNLNVALNR -----GINP-----GMLPHENV----- ●	ATA A A	V
MLGLRPSAERAPRPAVFPVAPATASRRPDGTRATRLRVMPEREDYENNVAY --DMR-SAITDW-----		VI
GVRLNLNPGVGVRQAVAAFTVDRAERPAAVANIRAALDPIASQFSQLRT -----SDMREAL-----		VII
ISKADAESEELGFKDAADHHTDDVTHCLFGGELSLSNPDQQVIGLAGNPT -----QHANGIHADIP----- ↑ CA40		VIII
DTSQPYSEQGNKDLAFMDMKKLAQFLAGKPEHPMTRETNAE . . . PSPERFVATMN-----PSGSIRMSTLSPS . . .		IX

FIG. 13A

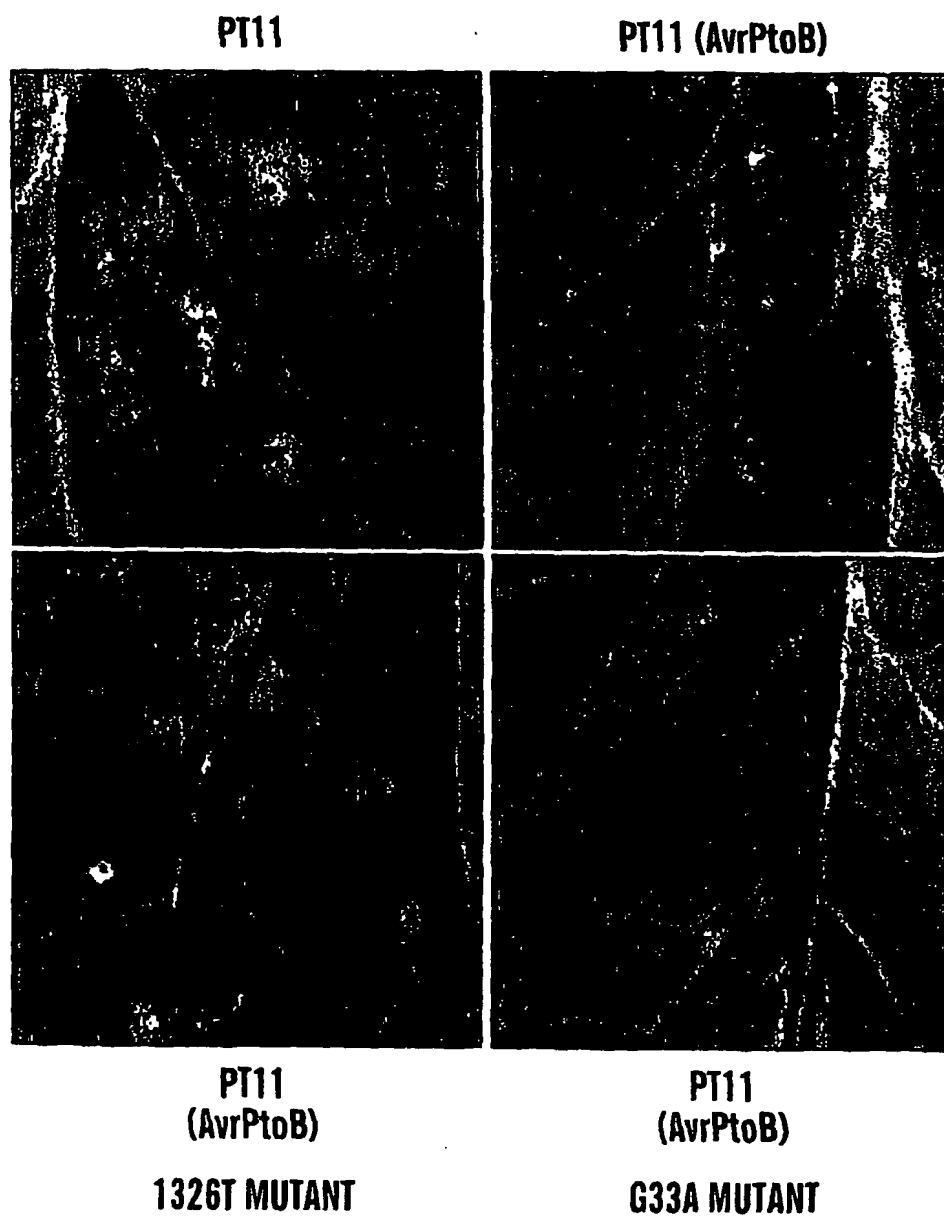
Consensus:		SxRxxLxxSxxLxRxxE	
AvrPto	38	SVRHQLAESAGLPRDQHE	55
AvrPtoB	60	TGRERLSRSTALSRQTRE	77
VirPphA	51	SGRQRLLRSSALSRQTRE	68
AvrRpt2	49	ETRALLATKTVLGRHKIE	66
AvrRps4	38	TTTSIAQASEGLQRPAT	55
AvrXa10	61	SPAFSAGSFGDLLRQFDP	78
AvrPpiB	41	IEEHVADRLSDLGRPDGG	58
AvrPphF	33	VGQYTLTSLHQLSSEERE	50
AvrBs1	49	RKRVIKENIAALHTSSLE	69
AvrB	33	SQRQLEVYDQCLIGAARW	50
AvrBsT	42	SPSQTSSAFSGLPERPRK	59

FIG. 13B

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**FIG. 14**

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ALL LEAVES ARE Rio-Grande PtoR(*Pto*/*Pto*)

FIG. 15

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